



## Research Article

# Identifying Priority Chronic Wasting Disease Surveillance Areas for Mule Deer in Montana

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**ABSTRACT** Chronic wasting disease (CWD) is a fatal prion disease that affects a variety of ungulate species including mule deer (*Odocoileus hemionus*). As of 2014, no CWD cases had been reported in free-ranging ungulates in Montana. However, nearby cases in Canada, Wyoming, and the Dakotas indicated that the disease was encroaching on Montana's borders. Mule deer are native and common throughout Montana, and they represent a significant portion of the total hunter-harvested cervids in the state. The arrival of CWD in Montana may have significant ecosystem and socioeconomic impacts as well as potential consequences for wildlife management. We used 18,879 mule deer locations from 892 individual deer collected during 1975–2011 and modeled habitat selection for 7 herds in 5 of the 7 wildlife management regions in Montana. We estimated resource selection functions (RSF) in a Bayesian framework to predict summer and winter habitat preferences for mule deer. We estimated deer abundance from flyover counts for each region, and used the RSF predictions as weights to distribute the deer across the region. We then calculated the distance to the nearest known infected herds. We predicted areas of high risk of CWD infection in mule deer as areas with densities above the median density estimate and within the lowest quartile of distances to known infected herds. We identified these areas, the southeast corner of Montana and the north-central border near Alberta and Saskatchewan, as priority areas for CWD surveillance and management efforts. Published 2015. This article is a U.S. Government work and is in the public domain in the USA.

**KEY WORDS** chronic wasting disease, disease surveillance, Montana, *Odocoileus hemionus*, resource selection, risk mapping.

Designing disease detection and management programs for wildlife populations can be challenging. Managers often want to detect diseases in the early stages, when the disease is rare, to exert control measures and prevent epidemics. However, the detection of rare events, such as the disease emergence in a population, often requires large expenditures of resources. Focusing disease surveillance efforts on subsets of the population that are more susceptible than others, for example using symptomatic animals (syndromic surveillance) or weighted surveillance (Walsh and Miller 2010), can reduce the effort required to obtain the desired probability of disease detection (Heisey et al. 2014). Identifying areas that contain animals at higher risk of disease because of potential contact with infected hosts is the first step in designing a cost-effective surveillance program.

Chronic wasting disease (CWD) is a disease affecting North American cervids including mule deer (*Odocoileus hemionus*), white-tailed deer (*Odocoileus virginianus*), elk (*Cervus elaphus*; Spraker et al. 1997), and Shiras moose (*Alces alces shirasi*; Baeten et al. 2007). A transmissible spongiform encephalopathy (TSE), CWD results in a lengthy (6–18 months) asymptomatic infectious period (Williams et al. 2002) while CWD prions accumulate in the body leading to eventual tissue damage and death (Almberg et al. 2011). The disease can have significant population-level impacts on deer, mainly through increased mortality rates (Dulberger et al. 2010). Multiple methods of transmission occur with CWD, including direct and indirect, but the current role of each of these transmission methods is poorly understood (Almberg et al. 2011). Additionally, CWD prions can remain infectious for years in soil (Miller et al. 2004, Johnson et al. 2007), making this disease difficult to manage once established. Early detection of CWD-infected deer may enhance the ability of managers to remove infected animals, limit environmental contamination, and slow the spread of the disease.

There is still much that is unknown regarding the transmission mechanism of CWD. There is no consensus

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in the current literature regarding whether CWD transmission is frequency-dependent or density-dependent (Joly et al. 2006, Oraby 2014). Storm et al. (2013) concluded that CWD transmission in young deer is likely driven by a combination of factors and that the relationship between deer density, frequency of disease, and disease incidence in young deer was non-linear. Regardless of transmission mechanisms, previous research has identified several risk factors that are associated with CWD. For example, Rees et al. (2012) determined that in Saskatchewan, CWD prevalence varied as a function of individual characteristics (species and sex), landscape characteristics (land cover, distance to water, terrain ruggedness), and temporal factors (river networks were more important in the early phase of disease spread). In that same study, mule deer were more likely to be CWD positive than white-tailed deer in the same areas (Habib 2011, Rees 2012). Habib et al. (2011) suggested that mule deer may be at greater risk of CWD than white-tailed deer because of their larger group sizes and greater overlap of home ranges, which leads to an increase in contact rates between conspecifics.

Currently, there have been no confirmed cases of CWD in the free-ranging cervid populations in Montana. Since 1998, more than 17,000 free-ranging ungulates, including approximately 10,000 mule deer, have been tested. However, CWD has been detected in mule deer as well as in other wild cervid species in the neighboring states of Wyoming, South Dakota, and North Dakota, as well as the Canadian provinces of Alberta and Saskatchewan directly north of the Montana border. A CWD epidemic in Montana could negatively affect hunting opportunities and ecosystems in the state. Approximately 150,000 people hunt deer, and between 35,000 and 65,000 mule deer have been harvested annually in the state during the last decade. Mule deer are a common, native species throughout the state that affect plants upon which they forage and serve as prey items for an intact large carnivore guild including mountain lions (*Puma concolor*), wolves (*Canis lupus*), coyotes (*Canis latrans*), black bears (*Ursus americanus*), and grizzly bears (*Ursus arctos*).

Predicting when and how a disease will emerge in a previously uninfected population is a daunting task, but surveillance efforts focused on areas of population overlap may improve the probability of detecting the disease in its early stages (Silbernagel et al. 2011). Mule deer range widely throughout Montana; therefore, delineating areas that are likely to be used by many animals and are in close proximity to infected herds in neighboring states can help predict where CWD may first be detected. Our objective was to systematically identify areas to prioritize for CWD surveillance in Montana. To accomplish this goal, we used information on mule deer habitat, densities, and distance to known infected herds to determine locations that are at highest risk for disease spread. We identified areas that contained mule deer habitat by developing resource selection function (RSF) models (Manly et al. 2002). We then used data from population surveys to estimate density and locations of known infections to estimate distance from the nearest infected herd to identify high-risk areas for CWD invasion.

## STUDY AREA

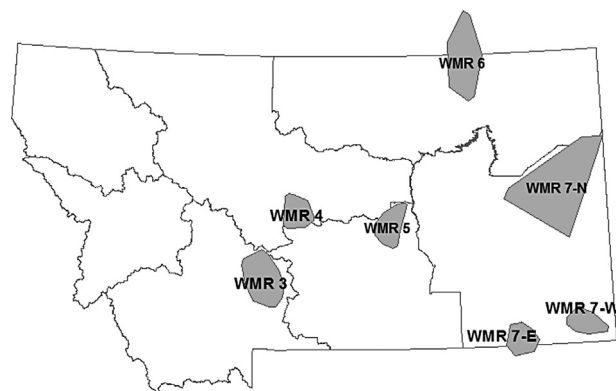
During 1975–2011, we obtained 18,879 mule deer locations via very high frequency (VHF) and global positioning system (GPS) telemetry from 892 individual deer. These deer were from 7 different herds in 5 of the 7 wildlife management regions (WMR) of Montana (Fig. 1). Deer were captured and collared in accordance with the standard biomedical handling protocol developed by Montana Fish, Wildlife and Parks (Montana Fish, Wildlife and Parks 2007). The herds ranged from the lower elevation grassland areas of Montana (WMR 4, 6, and 7) to predominantly mountainous regions (WMR 3 and 5). Average elevations for randomly selected locations in the summer ranged from 855 m in WMR 6 to 1,723 m in WMR 3 and in the winter from 811 m in WMR 6 to 1,764 m in WMR 3. Road density also varied between the regions; distance to the nearest road in summer at random locations ranged from 441 m in WMR 4 to 1,665 m in WMR 7-N. Wildlife management regions 4, 6, 7-E, and 7-W occupied areas with less forest cover (0–6% at random summer locations) than WMR 3, 5, and 7-N (21%, 40%, and 27%, respectively; see Table S1 available online at [www.wileylibrary.com](http://www.wileylibrary.com)). These 5 wildlife management regions contained approximately 90% of the delineated mule deer wintering habitat in Montana and the mule deer habitat that was adjacent to known CWD infections in neighboring jurisdictions.

## METHODS

We obtained aerial survey data from 46 mule deer survey units, surveyed from 1971 to 2011, throughout the same 5 WMRs. Mule deer are aerially surveyed throughout Montana in December and early spring (Mar–Apr; Newell 2013). During the spring surveys, biologists complete total counts for use as annual population trend indices (Newell 2013). We compiled the spring trend count records for the 46 survey units located in these wildlife management regions.

### Resource Selection

We used a use-available design based on mule deer VHF and GPS locations and random points to estimate the coefficients



**Figure 1.** Locations within wildlife management regions (WMRs) of mule deer herds with very high frequency (VHF) and global positioning system (GPS) data from 1975 to 2011, which we used to develop resource selection functions for the state of Montana.

of an exponential resource selection function with logistic regression (Johnson et al. 2006, Lele and Kiem 2006). We developed separate models for winter (Dec–Mar) and summer (Apr–Nov). The winter dates correspond to a period of relatively sedentary behavior when mule deer tend to cluster in matriarchal groups. The summer period corresponded to a period of movement during the spring, summer, and fall when deer continue to use the winter range but expand their movements to additional areas they do not use during winter. For our models, we defined available habitat separately for winter and summer by delineating the boundaries of each herd using minimum convex polygons (MCP), and buffering those boundaries by the maximum distance moved by an individual deer during the season. We calculated maximum distances moved for GPS-collared deer using the package *adehabitat* in R (Calenge 2006). For every used point, defined as a GPS or VHF location, we selected 10 random locations from the same herd, on the same day from within the buffered MCP (Turner et al. 2004, Proffitt et al. 2013). Covariates for used and available locations were on a 30-m by 30-m-pixel scale.

We formulated our logistic regression in a Bayesian framework using WinBUGS (Lunn 2000) and R2WinBUGS (Sturtz et al. 2005):  $\text{logit}(p) = \alpha + \beta \times X$ , where  $p$  is a binomial variable equal to 1 if the location was used and 0 if the location was available,  $\alpha$  is the intercept of the logistic regression,  $\beta$  are the coefficients, and  $X$  is a matrix of covariates. In our case  $\alpha$  is a herd-level random intercept and  $\beta$  are the herd-level random effects coefficients formulated in the standard fashion as normally distributed with a mean of  $\mu$  and precision  $\tau$  (1/variance; Gelman et al. 2004). We set uninformative priors on  $\mu$  using a normal distribution with a mean of 0 and a precision of 0.001. Priors on  $\tau$  were expressed as a function of the standard deviation  $\sigma$ , where  $\tau = 1/\sigma^2$ , and the prior on  $\sigma$  was set as an uninformative uniform distribution between 0 and 10. We ran models for 50,000 iterations with a burn in of 10,000 iterations. We assessed convergence by visual inspection of the chains, the Gelman–Rubin statistic and  $\hat{R}$  values using package *coda* (Plummer 2006).

Predictions based on unconditional (population-level) estimates represent predictions made for locations where nothing is known about herd identity. Predictions based on conditional estimates represent predictions made for locations where the herd identity is known. In other words, predictions made using the conditional estimates assume that deer in herds close to the herds used to develop the model have similar behavior. We evaluated whether conditional or unconditional estimates were better predictors of use using the methods of Johnson et al. (2006). These methods include withholding data, estimating an RSF with the training data, binning the predicted RSF values, determining the midpoint value of each bin, and determining the observed use of each bin using the equation  $U(x_i) = w(x_i) \times A(x_i) / \sum_j w(x_j) \times A(x_j)$ , hereafter referred to as Eq. 1 (Boyce and McDonald 1999) where  $w(x_i)$  is the midpoint RSF of bin  $i$  and  $A(x_i)$  is the area of bin  $i$ . We then predicted the RSF values for the withheld data, counted the number of used observations from the withheld data in each bin, and

calculated the expected number of observations in each RSF bin ( $i$ ) using the equation,  $N = N_i \times U(x_i)$ , hereafter referred to as Eq. 2 (Boyce and McDonald 1999) where  $N$  is the total number of deer locations in the withheld data set. Note that when making predictions from an exponential RSF, the intercept is dropped (Boyce and McDonald 1999, Gillies et al. 2006). Therefore, we calculated RSF predictions for each pixel ( $p_j$ ) as  $p_j = \exp(\beta X_j)$ . We then compared the expected number to the observed number of deer locations in each RSF bin using  $\chi^2$  tests and a regression where the expected slope is 1 and the expected intercept is 0. To evaluate unconditional estimates, we withheld data from an entire herd and predicted for RSF values for the whole herd. For conditional estimates, we performed k-folds cross validation and divided the data set into 10 sections. We repeated the Johnson et al. (2006) evaluation method 10 times for each herd, and we calculated the number of times the slope was not different from 1 and the intercept was not different from 0, along with the mean  $R^2$  values (Johnson et al. 2006). In addition, we report the percentage of used points with RSF values above the median value and 75th percentile of all RSF values (Durner et al. 2009, Proffitt et al. 2013) to provide an evaluation of whether high RSF values corresponded to observed used locations.

### Covariates

We included the following covariates in the RSF: normalized difference vegetation index (NDVI, an index of productivity; Bartlette et al. 2006), temperature, precipitation, land cover, distance to road, elevation, slope, and aspect, all of which are known to affect mule deer habitat use in Montana (Mackie et al. 1998). We obtained land cover types on a 30-m resolution from the 2006 national land cover data set ([www.mrlc.gov](http://www.mrlc.gov)), and characterized each type as forest, dry land (including sage brush and steppe), grassland, aquatic (wetlands and other riparian zones), and other (including developed lands). We obtained road data from the United States Census Bureau 2000 TIGER files, and elevation, slope, and aspect data from the National Elevation data set (NED; Gesch 2009) on a 30-m resolution. We obtained NDVI values from a 1-km resolution weekly averaged NDVI data layer that was corrected for cloud cover (Bartlette et al. 2006, <http://www.wfas.net/>). The original NDVI layer was developed by EROS (<https://lta.cr.usgs.gov/emodis>) on a MODIS platform. We extracted daily temperature and precipitation data from PRISM (Gibson et al. 2002, <http://www.prism.oregonstate.edu/>) on a 1-km resolution. We matched temperature and precipitation data to used and random locations by the specific day of use, and matched NDVI by the week of use. We standardized all covariates prior to analyses to have a mean of 0 (i.e., we subtracted the mean of the covariate from the observed value of the covariate and divided this quantity by the standard deviation of the covariate).

We developed candidate models based on 4 categories of covariates: 1) climate (including temperature, precipitation, and NDVI), 2) terrain (elevation and slope), 3) vegetation cover (including all categories of cover), and 4) roads for both summer and winter. We compared 14 models containing all

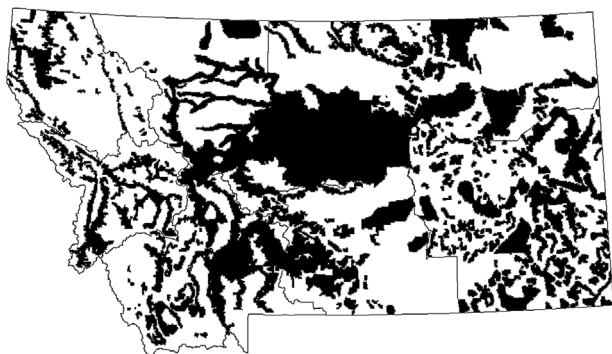
combinations of the 4 categories using Deviance Information Criterion (DIC; Spiegelhalter et al. 2002, see Table S2 available online at [www.wileylibrary.com](http://www.wileylibrary.com)).

### Identification of High-Risk Areas

Once we identified our best-fit RSFs for both seasons, we predicted the RSF value for both winter and summer for a 30-m pixel placed at each centroid of a 1-km<sup>2</sup> grid overlaid on the 5 WMRs in which our data were collected. We selected the 1-km<sup>2</sup> pixel as an area unit large enough to be meaningful to deer movements (largest estimated daily movements were 13 km) and small enough to capture the variability in the landscape. We sampled covariates on a 30-m pixel across the state of Montana in a 1-km grid resulting in approximately 3,00,000 sampling points. We predicted the RSF value for each point and the rasterized the predicted values on the 1-km<sup>2</sup> by taking the mean value of all predicted locations inside the area identified by Montana Fish, Wildlife and Parks wildlife biologists as mule deer winter range (Fig. 2). We buffered the winter range using the maximum distance moved in a day in the summer (13 km) and predicted the RSF values for the summer habitat using the same method.

We used aerial survey data to estimate the number of deer per herd for 2010–2012, and then estimated densities of deer for each surveyed herd by dividing the estimated count by the survey area to obtain number/km<sup>2</sup>. For areas where densities were unknown (i.e., there were no surveyed deer herds in the area), we used the mean estimate of deer per herd in the wildlife management region. We then summed the densities per 1-km<sup>2</sup> pixel to obtain a total number of deer for each WMR ( $N$ ). We calculated relative use using Eq. 1, and the number of animals expected in each habitat type using Eq. 2 (Boyce and McDonald 1999). The density of animals in the  $i$ th habitat is calculated as  $D(x_i) = N \times U(x_i)$  and the number of animals is estimated by  $\hat{N}' = \sum_j D(x_j) \times A'(x_j)$  (Boyce and McDonald 1999:Box. 2). We did not predict deer densities for lands under tribal jurisdiction or belonging to the United States National Park Service.

To estimate the proximity of deer to infected herds, we calculated the distance from the centroid of each 1-km<sup>2</sup> pixel in Montana to the nearest known infected herd in neighboring jurisdictions ([www.cwd-info.org](http://www.cwd-info.org), accessed 26 May 2015). We downloaded hunting district maps from the



**Figure 2.** Mule deer winter range (1975–2011) in the state of Montana delineated by Montana Fish, Wildlife and Parks wildlife biologists.

**Table 1.** Model selection results for both winter and summer resource selection of mule deer in Montana, 1975–2011. DIC = Deviance Information Criterion; NDVI = Normalized Difference Vegetation Index.

Model	DIC	ΔDIC
Winter model		
Elevation, elevation × elevation, cover type, distance to road	32,600	0
Elevation, elevation × elevation, cover type	32,822	222
Elevation, elevation × elevation	33,404	804
Cover type	33,966	1,366
Summer model		
Elevation, cover type, distance to road	27,015	0
Elevation	27,048	33
Cover type, precipitation, temperature, NDVI	27,642	627
NDVI, temperature, precipitation	27,927	912
Cover type	27,971	956

websites of neighboring states and provinces ([www.AltalIS.com](http://www.AltalIS.com), <http://wgfd.wyo.gov/web2011/wildlife-1000819.aspx>, <http://www.environment.gov.sk.ca>, <http://esrd.alberta.ca/forms-maps-services/maps/map-distribution-centre>) to help with the identification of areas with infected herds. Finally, to identify areas of highest relative risk, we selected 1-km<sup>2</sup> pixels with estimated densities above the median value (the top 50% of the density estimates) and with an estimated distance to the nearest infected herd in the lowest 25% of all estimated distances (bottom quartile).

## RESULTS

The best models of winter and summer habitat selection contained the covariates elevation, elevation squared, vegetation cover, and distance to road (Table 1). Availability of these covariates in areas where the winter model was developed was approximately similar to availability in the areas where we predicted RSF values in winter and summer (Table 2). Models converged with  $\hat{R}$  values of approximately 1. Slope was highly correlated with elevation ( $r = 0.85$ ) and thus, removed from our analyses. No other models were

**Table 2.** Summary statistics for development and prediction data sets for resource selection functions (RSFs) of mule deer habitat selection in Montana (1975–2011).

Covariates	Development set	Prediction set
Winter		
Elevation (m; mean)	1,313 (SD 417)	1,154 (SD 392)
Distance to road (m; mean)	1,140 (SD 1,436)	943 (SD 1,086)
Grass (%)	39	33
Forest (%)	15	14
Dryland (shrub and steppe) (%)	33	37
Summer		
Elevation (m; mean)	1,428 (SD 434)	1,205 (SD 495)
Distance to road (m; mean)	879 (SD 1,121)	974 (SD 1,433)
Grass (%)	29	29
Forest (%)	17	14
Dryland (shrub and steppe) (%)	31	24

**Table 3.** Parameter estimates from the best model of winter ( $n=861$  deer) and summer ( $n=641$  deer) mule deer habitat selection from 7 deer herds in Montana between 1975–2011. Covariates were standardized prior to analysis. LCL indicates the lower 95% credible limit, UCL indicates the upper 95% credible limit, and median indicates the 50th percentile of population-level  $\beta$  estimates.

Parameter	Winter			Summer		
	LCL	median	UCL	LCL	median	UCL
Intercept	−7.49	−2.89	1.78	−5.33	−1.68	1.75
Elevation (m)	−10.78	−4.01	2.55	−4.51	1.67	7.21
Elevation $\times$ elevation ( $m^2$ )	−13.72	−6.83	−0.11	−6.57	−1.23	3.45
Distance to road (m)	−0.18	0.48	1.16	−0.20	0.35	0.94
Drylands (shrub, steppe) (%)	−3.28	−0.20	2.8	−0.56	0.36	1.30
Forest (%)	−3.79	−0.77	2.23	−0.73	0.03	0.85
Grasslands (%)	−3.09	0.03	3.18	−0.59	0.45	1.50

within 10 DIC points of the top model. Unconditional parameter estimates revealed variable relationships between habitat selection and covariate values among herds (Table 3). Ninety percent of the posterior estimates for distance to road were above 0, indicating that mule deer were avoiding roads, but the 95% credible interval of the population-level estimate of the distance to road parameter contained 0. The combination of a weak positive effect of elevation and a strong negative effect of elevation squared (95% credible interval does not include 0) indicates selection for mid-range elevation during the winter months. Inspection of conditional parameter estimates for each herd used to develop the models revealed considerable among-herd variation in parameter estimates (Table 4). For example, the median estimate for the effect of elevation ranged from −27 for WMR 4 to 6 for WMR 7-N.

Unconditional estimates (the overall mean of the random effect value assuming the herd was unknown) made by withholding all data from a herd and predicting RSF values for the withheld herd predicted use poorly (Table 4). Intercepts and slopes between predicted number of locations

in selection bins and observed use in the bins were different from 0 for 5 out of 7 herds in winter and 7 out of 7 herds in summer.  $R^2$  values were  $<0.50$  for 6 out of 7 herds in winter and  $<0.0$  for 4 out of 7 herds in winter; in summer,  $R^2$  values were  $<0.50$  for 5 out of 7 herds and 0.0 for 2 out of 7 herds. Only 2 out of 7 herds had  $>70\%$  of used points with RSF values above the median value in winter and summer, and only 3 out of 7 had  $>40\%$  of used points with RSF values above the 75th percentile in winter and 2 out of 7 in summer. Chi-square tests revealed statistically significant differences for all (unconditional and conditional) models ( $P < 0.001$ ), but these results were clouded by our large sample sizes (i.e., small differences were statistically significant).

Our model evaluation revealed generally adequate fits to the data for conditional estimates (Table 4). Overall  $R^2$  values were  $>0.75$  for 6 out of 7 herds in the winter months and 5 out of 7 herds in the summer months. The exception was the WMR 5 herd, which had  $R^2$  values  $<0.40$ . At least 5 out of 10 intercepts and slopes were not statistically different from 0 or 1, respectively, for all herds in winter and summer. For all herds except the herd in WMR 5,  $>70\%$  of the used

**Table 4.** Results of model evaluation for resource selection functions (RSFs) developed for mule deer in Montana, 1975–2011. We evaluated conditional estimates with k-folds cross validation using herd-level parameter estimates to predict for withheld data (10 separate times for 10 sets of withheld data). We evaluated unconditional estimates by withholding all the data from 1 herd, running the model and predicting for the withheld herd using the global mean coefficient estimates. For conditional estimates, WMR = wildlife management region; Int = the number of intercepts (out of 10) not statistically different from zero; Slopes = the number of slopes (out of 10) not statistically different from 0, Mean  $R^2$  = the average  $R^2$  value (among the 10 herds),  $>50\%$  = the percentage of used points with RSF values above the median, and  $>75\%$  = the percentage of used points with RSF values above the 75th percentile. For unconditional estimates, Int = whether the estimated intercept was different from 0; Slope = whether the estimated slope was different from 0;  $R^2$  = the  $R^2$  value;  $>50\%$  = the percentage of used points with RSF values above the median, and  $>75\%$  = the percentage of used points with RSF values above the 75th percentile.

WMR	Conditional estimates (k-folds cross validation)					Unconditional estimates				
	Int	Slopes	Mean $R^2$	$>50$ (%)	$>75$ (%)	Int	Slope	$R^2$	$>50$ (%)	$>75$ (%)
Winter										
3	10	6	0.96	83	66	Yes	Yes	−0.08	69	35
4	10	10	0.79	83	44	No	Yes	−0.09	72	42
5	10	10	0.32	80	54	Yes	Yes	0.03	42	9
6	7	7	0.91	73	44	Yes	Yes	−0.09	39	23
7-East	10	10	0.85	94	64	No	No	0.42	58	41
7-North	10	10	0.97	54	34	Yes	No	0.72	81	74
7-West	7	8	0.78	92	72	Yes	Yes	−0.03	53	16
Summer										
3	7	7	0.98	93	76	Yes	Yes	0.00	19	7
4	8	8	0.91	86	59	Yes	Yes	0.26	45	21
5	10	10	0.18	57	29	Yes	Yes	0.27	19	2
6	5	7	0.89	85	64	Yes	Yes	0.71	90	55
7-East	9	9	0.77	76	41	Yes	Yes	0.27	40	10
7-North	10	10	0.70	87	72	Yes	Yes	0.00	18	7
7-West	5	5	0.95	74	50	Yes	Yes	0.95	97	81

locations had values above the median RSF value in both summer and winter and >40% of used points had RSF values above the 75th percentile of RSF values. However, even for the herd in WMR 5, >50% of points were above the median and greater than 25% of points were above the 75th percentile.

Based on these results, we divided the state of Montana into areas that corresponded to the locations of the herds (Fig. 1) used to build the models, and used conditional estimates to predict RSF values (Table 5). For region 7, we divided the region into 3 sections, north, east, and west corresponding to the locations of the 3 herds in region 7 used in model development. For all other regions, we used the regional boundaries (e.g., we predicted RSF values for WMR 3 using the estimates from the herd used to develop the RSF from that region).

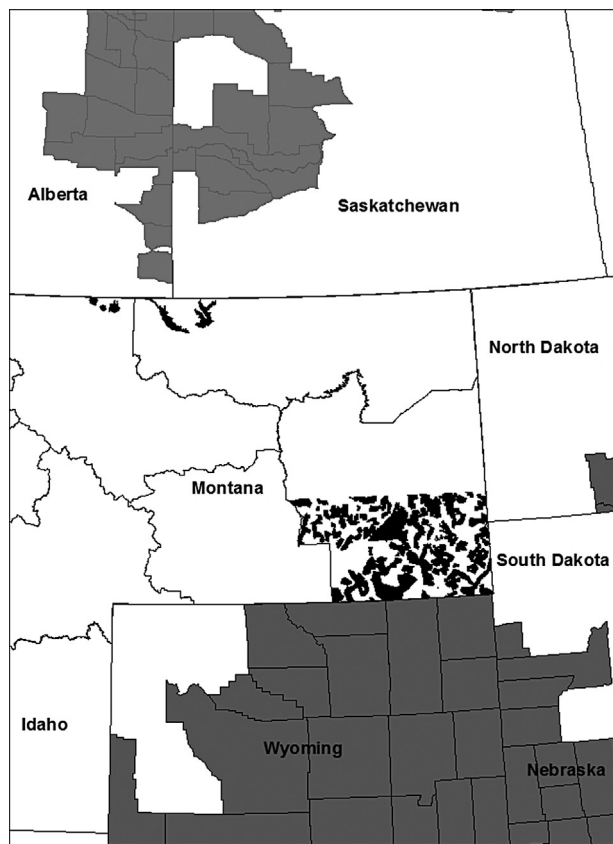
Summer and winter areas of highest relative disease risk were similar (Figs. 3 and 4). Areas identified as high risk were predicted to have high deer densities (relative to the rest of the state) and be close to the known distribution of infected deer. We identified the southeast corner of Montana located near the border of Wyoming, North Dakota, and South Dakota, and 2 areas in the central-northern part of Montana near the provinces of Alberta and Saskatchewan as high risk in both winter and summer. We identified an additional area of high summer risk just north of western Wyoming, north of the eastern border of Yellowstone National Park.

## DISCUSSION

We identified high-risk areas in the southeastern and north-central areas of Montana that contained high deer densities and were relatively close to known infected herds. This

**Table 5.** Conditional parameter estimates from the best models of resource selection for mule deer from 7 herds in Montana, 1975–2011. WMR indicates the wildlife management region (3–7) that the estimates are associated with. LCL=lower 95% credible limit, UCL=upper 95% credible limit, med = median value.

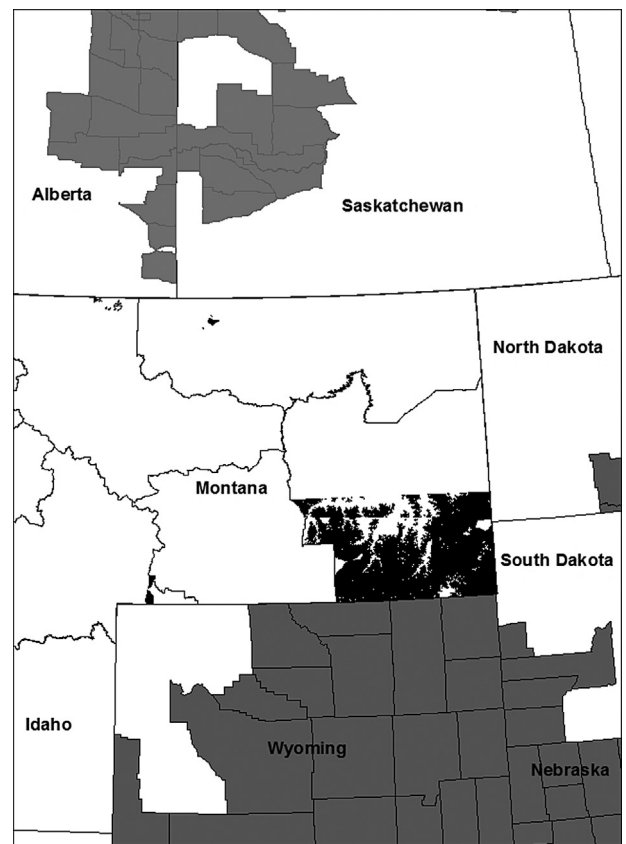
			WMR						
Parameter			3	4	5	6	7-E	7-N	7-W
Winter									
Intercept	LCL		−11.32	−7.29	−4.09	−2.20	−6.64	−2.19	4.54
	med		−7.62	−5.99	−3.85	−1.82	−6.03	−1.35	6.35
	UCL		−3.89	−4.49	−3.61	−1.46	−5.46	−0.31	8.90
Elevation (m)	LCL		−14.17	−33.00	0.87	0.28	4.96	−0.48	−6.39
	med		−7.44	−27.17	1.15	1.94	6.07	2.10	−4.10
	UCL		−0.55	−20.71	1.44	3.42	7.28	5.25	−0.03
Elevation × Elevation (m <sup>2</sup> )	LCL		−5.56	−44.42	−0.73	1.42	−4.27	−0.31	−9.55
	med		−2.59	−37.95	−0.62	3.71	−3.67	1.63	−8.07
	UCL		0.4	−30.78	−0.51	5.75	−3.12	4.02	−5.59
Distance to Road (m)	LCL		0.34	−0.22	0.92	1.12	−0.76	0.57	0.51
	med		0.39	−0.14	0.99	1.29	−0.46	0.83	0.54
	UCL		0.44	−0.05	1.06	1.45	−0.18	1.07	0.58
Drylands (%)	LCL		1.36	−0.78	1.45	−0.13	1.68	−0.12	−8.66
	med		1.63	−0.58	1.63	0.15	2.19	0.12	−6.52
	UCL		1.90	−0.38	1.82	0.44	2.74	0.36	−5.12
Forest (%)	LCL		−0.19	−0.81	0.90	−0.16	0.90	−0.51	−9.26
	med		0.07	−0.59	1.10	0.11	1.38	−0.19	−7.14
	UCL		0.32	−0.38	1.30	0.39	1.91	0.14	−5.72
Grasslands (%)	LCL		1.28	0.03	1.71	−0.26	1.62	−0.24	−8.64
	med		1.78	0.54	1.90	0.04	2.12	0.33	−6.45
	UCL		2.26	1.04	2.1	0.33	2.69	0.85	−5.03
Summer									
Intercept	LCL		−4.32	−4.15	−3.18	−5.94	−6.36	2.43	−1.73
	med		−4.16	−3.75	−1.40	−4.19	−3.39	5.52	−0.86
	UCL		−4.00	−3.41	0.29	0.32	−0.29	7.12	−0.05
Elevation (m)	LCL		1.61	2.78	−1.90	−1.08	−19.54	5.41	−1.65
	med		1.82	3.46	2.11	1.61	−11.30	11.12	1.36
	UCL		2.02	4.21	5.88	8.55	−2.89	14.04	4.14
Elevation × Elevation(m <sup>2</sup> )	LCL		−0.45	−3.73	−0.79	0.75	−17.50	0.49	−2.15
	med		−0.38	−3.18	1.48	1.90	−11.66	2.99	0.30
	UCL		−0.31	−2.67	3.57	4.53	−5.98	4.31	2.54
Distance to Road (m)	LCL		0.55	−0.78	0.38	0.36	−0.13	0.39	0.91
	med		0.60	−0.59	0.59	0.41	−0.06	0.43	1.06
	UCL		0.64	−0.40	0.82	0.45	0.00	0.46	1.20
Drylands (%)	LCL		0.40	0.73	−0.15	1.30	−1.05	0.50	−0.85
	med		0.53	1.09	0.10	1.51	−0.85	0.73	−0.58
	UCL		0.68	1.45	0.35	1.71	−0.65	0.96	−0.32
Forest (%)	LCL		0.25	0.87	−0.84	0.15	−1.26	0.12	−0.77
	med		0.39	1.20	−0.47	0.31	−1.05	0.32	−0.52
	UCL		0.55	1.56	−0.11	0.48	−0.84	0.54	−0.26
Grasslands (%)	LCL		0.83	0.56	−1.57	1.24	−0.26	0.17	−0.88
	med		0.97	0.92	−0.79	1.92	0.28	0.61	−0.61
	UCL		1.11	1.31	−0.12	2.58	0.82	1.03	−0.34



**Figure 3.** High priority areas for chronic wasting disease (CWD) surveillance in the state of Montana, identified based on predictions of winter habitat use of mule deer from resource selection functions and distance to nearest known infected herd using data from 1975–2011. Areas in black represent areas with above median estimates of mule deer densities and within the lowest quartiles of distances from the nearest infected herd. Areas in gray represent counties in the United States and wildlife management units in Canadian provinces where CWD has been detected.

information will be used to guide the wildlife management agency in the state of Montana to enhance surveillance and management efforts. Early detection of CWD could provide wildlife managers with a broader range of potential management tools, such as culling and/or restrictions on carcass movements on the state or wildlife management unit scale, and increase the likelihood that actions aimed at controlling the disease will be successful. Predicting the rate and geographic distribution of disease spread is difficult because of lack of knowledge regarding methods of transmission, environmental restrictions on the disease (Daszak et al. 2013), behavioral differences in a species across its range, variable host susceptibility (Beldomenico and Begon 2010), and a variety of other factors. Early detection of disease is vital to implementing control and/or eradication strategies (Ferguson et al. 2014). Properly designed surveillance programs can assist with the early detection of disease (Nusser et al. 2007), and identifying individuals and populations at the greatest risk of contracting a disease is the first step in designing a cost-effective surveillance program (Walsh and Miller 2010).

Our unconditional parameter estimates could not accurately predict RSF values for unknown herds, and our



**Figure 4.** High priority areas for chronic wasting disease (CWD) surveillance in the state of Montana, identified based on predictions of summer habitat use of mule deer from resource selection functions and distance to nearest known infected herd using data from 1975 to 2011. Areas in black represent areas with above median estimates of mule deer densities and within the lowest quartiles of distances from the nearest infected herd. Areas in gray represent counties in the United States and wildlife management units in Canadian provinces where CWD has been detected.

conditional estimates varied widely among herds. This implies that herd-level differences in resource selection are high, which makes it difficult to predict use across the entire Montana landscape. In particular, in WMR 5 we found that even conditional RSF values did not have high correlation with use, likely because there was little difference between used and available points in this area, which contains relatively ubiquitous, high quality deer habitat. Ideally, multiple herds from each region could be used to produce a fixed-effect model for the local area. Mule deer are adaptable generalists, in which case broad-scale RSFs may have limited utility in predicting areas of high use in new herds. At a minimum, predictive ability of broad-scale RSF models should be validated before such models are used to inform conservation or management decisions.

Although we found that locally-based predictions of RSF values were more accurate in predicting local mule deer distribution, application of local RSF model predictions over large areas also can be problematic. The primary shortcomings of such an approach lie in delineating boundaries within which particular data and models should be used to predict, and in the cost of developing local predictions with local data. The issue of poor predictive capacity of RSF

models based on data from different habitat or ecotypes than those for which predictions are made is common (e.g., Proffitt et al. 2013). In our case, we used administrative boundaries combined with proximity to collared animal locations to define which data we used to develop RSFs to predict mule deer selection for given areas. The use of WMRs to develop RSFs was a reasonable approach in Montana, where mule deer management is largely organized around 5 major ecotypes (Montana Fish, Wildlife and Parks 2001), the boundaries of which generally align with the WMR boundaries. In other situations, the boundaries within which to develop RSFs may not be as clear and may need to be investigated.

Statistically valid surveillance studies are important for identifying new diseases or disease emerging in new geographic areas. One approach to identifying high-risk areas for CWD infection involves using logistic regression and positive and negative CWD-tested animals, along with spatial covariates, to estimate the probability of infection (Walsh and Otis 2012). This approach also can make use of non-spatial data on demographic factors associated with the risk of infection to develop optimal spatial and demographic surveillance strategies (Walsh and Miller 2010, Walsh and Otis 2012, Heisey et al. 2014). However, application of this approach to uninfected areas, such as Montana, is problematic because the lack of positive test cases precludes development of a local risk of infection model. The approach we used based on local deer location and survey data combined with the location of nearby infections is therefore more likely to be reliable locally, which is important for informing the development of local surveillance and management strategies.

## MANAGEMENT IMPLICATIONS

Focusing surveillance efforts prior to disease emergence in a particular geographic area can be accomplished by identifying risk factors associated with disease in other areas. For CWD, identifying locations with high deer densities close to infected deer herds can be an effective first step for identifying priority areas for surveillance programs. We identified such areas in Montana, which the state of Montana can use to develop a design-based CWD surveillance program. Montana Fish, Wildlife and Parks also can focus surveillance on these high-risk priority areas to provide for the earliest detection possible given an affordable sampling effort. Our approach may also be useful in other jurisdictions with CWD encroaching on their borders or expanding in distribution. Early detection of disease in a new location can increase the ability of wildlife managers to mitigate the impacts of the disease or control the spread of the disease geographically.

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